Page 1 of 2



Blast 2 Sequences results

PubMed

Entrez

BLAST

MIMO

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.13 [Nov-27-2005]

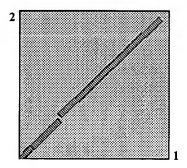
| Matrix BLOSUM62 ▼ | gap open: 11 | gap extension: | 1 | | | |
|--------------------------|-----------------|----------------|-------------|--------------|---------|---|
| x_dropoff: 50 expect: 1 | 0.000 wordsize | 3 Filter | View option | Standard | | Y |
| Masking character option | (for protein, n | for nucleotide | Masking | color option | Black 💌 | |
| Show CDS translation | Align | | | | | |

Sequence 1: lcl|seq_1 Length = 183 (1 .. 183)

Sequence 2: gi|1717863|sp|P52491|UBC12_YEAST|NEDD8-conjugating enzyme UBC12 (RUB1-conjugating enzyme) (RUB1-protein ligase) (Ubiquitin carrier protein 12).

Length = 188 (1 .. 188)





NOTE:Bitscore and expect value are calculated based on the size of the nr database.

```
Score = 153 bits (386), Expect = 5e-36
Identities = 76/179 (42%), Positives = 114/179 (63%), Gaps = 8/179 (4%)
           MIKLFSLKQQKKEEESAGGTKGSSKKASAAQLRIQKDINELNLPKTCDISF-
Query 1
           M+KL L+++K++E
                                      SAA++R+++D++ L+LP T ++
           MLKLRQLQKKKQKENE--NSSSIQPNLSAARIRLKRDLDSLDLPPTVTLNVITSPDSADR
Sbjct 1
                                                                        58
Query
           DDLLNFKLVICPDEGFYKSGKFVFSFKVGQGYPHDPPKVKCETMVYHPNIDLEGNVCLNI 114
                 ++++ PDEG+Y G F+
                                       + YP +PPKV C ++HPNIDL+GNVCLNI
Sbjct
      59
           SQSPKLEVIVRPDEGYYNYGSINFNLDFNEVYPIEPPKVVCLKKIFHPNIDLKGNVCLNI
Query 115
           LREDWKPVLTINSIIYGLQYLFLEPNPEDPLNKEAAEVLQNNRRLFEQNVQRSMRGGYI
           LREDW P L + SII GL +LFLEPNP DPLNK+AA++L
                                                     + F + V+ +M GG T
Sbjct 119
           LREDWSPALDLQSIITGLLFLFLEPNPNDPLNKDAAKLLCEGEKEFAEAVRLTMSGGSI
```

```
CPU time: 0.02 user secs. 0.00 sys. secs 0.02 total secs.

Lambda K H
0.318 0.138 0.411

Gapped
Lambda K H
0.267 0.0410 0.140
```

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Sequences: 1 Number of Hits to DB: 302 Number of extensions: 163

Number of successful extensions: 2
Number of sequences better than 10.0: 1
Number of HSP's gapped: 1
Number of HSP's successfully gapped: 1
Length of query: 183
Length of database: 1,238,154,749
Length adjustment: 125
Effective length of query: 58
Effective length of database: 1,238,154,624
Effective search space: 71812968192
Effective search space used: 71812968192
Neighboring words threshold: 9
X1: 16 (7.3 bits)
X2: 129 (49.7 bits)
X3: 129 (49.7 bits)
S1: 41 (21.7 bits)
S2: 74 (33.1 bits)

N

```
RESULT 1
UBE2M HUMAN
                                   PRT;
ID
     UBE2M HUMAN
                    STANDARD;
                                           183 AA.
     P61081; 076069; Q8VC50;
AC
     28-FEB-2003 (Rel. 41, Created)
DT
DT
     28-FEB-2003 (Rel. 41, Last sequence update)
DT
     10-MAY-2005 (Rel. 47, Last annotation update)
DE
     Ubiquitin-conjugating enzyme E2 M (EC 6.3.2.19) (Ubiquitin-protein
DE
     ligase M) (Ubiquitin carrier protein M) (Nedd8-conjugating enzyme
DΕ
     Ubc12).
GN
     Name=UBE2M; Synonyms=UBC12;
OS
     Homo sapiens (Human).
OC
     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC
     Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC
     Homo.
OX
     NCBI_TaxID=9606;
RN
     [1]
RP
     NUCLEOTIDE SEQUENCE.
RC
     TISSUE=Placenta;
RA
     Gong L., Yeh E.T.H.;
RT
     "Identification of the activating and conjugating enzymes of the
RT
     NEDD8-conjugation pathway.";
RL
     Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
RN
     [2]
     NUCLEOTIDE SEQUENCE.
RP
RX
     MEDLINE=98361870; PubMed=9694792;
RA
     Osaka F., Kawasaki H., Aida N., Saeki M., Chiba T., Kawashima S.,
     Tanaka K., Kato S.;
RA
RT
     "A new NEDD8-ligating system for cullin-4A.";
RL
     Genes Dev. 12:2263-2268 (1998) ...
RN
RP
     NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RA
     Kalnine N., Chen X., Rolfs A., Halleck A., Hines L., Eisenstein S.,
RA
     Koundinya M., Raphael J., Moreira D., Kelley T., LaBaer J., Lin Y.,
RA
     Phelan M., Farmer A.;
RT
     "Cloning of human full-length CDSs in BD Creator(TM) system donor
RT
     vector.";
     Submitted (MAY-2003) to the EMBL/GenBank/DDBJ databases.
RL
RN
RP
     NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RC
     TISSUE=Skin;
RX
     MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
     Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA
RA
     Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA
     Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA
     Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA
     Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
     Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA
RA
     Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA
     Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
     Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA
RA
     Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
     Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA
RA
     Fahey J., Helton E., Ketteman M., Madan A., Rodriques S., Sanchez A.,
RΑ
    Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA
     Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
     Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA
```

```
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA
RA
     Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT
     "Generation and initial analysis of more than 15,000 full-length human
RT
     and mouse cDNA sequences.";
RL
     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
     -!- FUNCTION: Catalyzes the covalent attachment of ubiquitin-like
CC
CC
        protein NEDD8 to other proteins.
CC
     -!- CATALYTIC ACTIVITY: ATP + ubiquitin + protein lysine = AMP +
CC
        diphosphate + protein N-ubiquityllysine.
CC
     -!- PATHWAY: Ubiquitin conjugation; second step.
CC
     -!- SIMILARITY: Belongs to the ubiquitin-conjugating enzyme family.
CC
CC
    This Swiss-Prot entry is copyright. It is produced through a collaboration
    between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC
CC
     the European Bioinformatics Institute. There are no restrictions on its
CC
    use as long as its content is in no way modified and this statement is not
CC
    removed.
CC
DR
     EMBL; AF075599; AAC26141.1; -; mRNA.
DR
     EMBL; AB012191; BAA33145.1; -; mRNA.
DR
     EMBL; BT006754; AAP35400.1; -; mRNA.
DR
    EMBL; BC058924; AAH58924.1; -; mRNA.
DR
    PDB; 1TT5; X-ray; E/F=1-26.
DR
    PDB; 1Y8X; X-ray; A=27-183.
DR
    SMR; P61081; 27-183.
DR
    Ensembl; ENSG00000130725; Homo sapiens.
DR
    HGNC; HGNC:12491; UBE2M.
DR
    MIM; 603173; -.
DR
    InterPro; IPR000608; UBQ-conjugat E2.
DR
    Pfam; PF00179; UQ_con; 1.
    ProDom; PD000461; UBQ_conjugat; 1.
DR
DR
    SMART; SM00212; UBCc; 1.
DR
    PROSITE; PS00183; UBIQUITIN CONJUGAT 1; 1.
DR
    PROSITE; PS50127; UBIQUITIN CONJUGAT 2; 1.
KW
    3D-structure; Ligase; Multigene family; Ubl conjugation pathway.
FT
    ACT_SITE
                                Glycyl thioester intermediate (By
                111
                      111
FT
                                similarity).
SO
    SEQUENCE
               183 AA; 20900 MW; E3C288CA6A98BC5C CRC64;
Alignment Scores:
Pred. No.:
                      9.77e-81
                                    Length:
                                                  183
Score:
                      970.00
                                    Matches:
                                                  183
                      100.0%
Percent Similarity:
                                    Conservative:
                                                  0
Best Local Similarity:
                      100.0%
                                    Mismatches:
                                                  0
Query Match:
                      96.3%
                                    Indels:
                                                  0
DB:
                                    Gaps:
                                                   0
US-10-681-690-3 (1-552) x UBE2M HUMAN (1-183)
           Qу
             1 MetIleLysLeuPheSerLeuLysGlnGlnLysLysGluGluGluSerAlaGlyGlyThr 20
Db
          61 AAGGGCAGCAAGAAGACGCCTCGGCGCGCGCGCGCTCCAGAAGGACATAAACGAC 120
Qу
             Db
          21 LysGlySerSerLysLysAlaSerAlaAlaGlnLeuArgIleGlnLysAspIleAsnGlu 40
```

| | Qy . | 121 | CTGAACCTGCCCAAGACGTGTGATATCAGCTTCTCAGATCCAGACGACCTCCTCAACTTC | 180 |
|---|-----------------|-----|--|-----|
| | Db | 41 | LeuAsnLeuProLysThrCysAspIleSerPheSerAspProAspAspLeuLeuAsnPhe | 60 |
| | Qy | 181 | AAGCTGGTCATCTGTCCTGATGAGGGCTTCTACAAGAGTGGGAAGTTTGTGTTCAGTTTT | 240 |
| | Db | 61 | LysLeuValIleCysProAspGluGlyPheTyrLysSerGlyLysPheValPheSerPhe | 80 |
| | Qy | 241 | AAGGTGGGCCAGGGTTACCCGCATGATCCCCCCAAGGTGAAGTGTGAGACAATGGTCTAT | 300 |
| | Db · | 81 | LysValGlyGlnGlyTyrProHisAspProProLysValLysCysGluThrMetValTyr | 100 |
| | Qy | 301 | CACCCCAACATTGACCTCGAGGGCAACGTCTGCCTCAACATCCTCAGAGAGGACTGGAAG | 360 |
| | Db | 101 | HisProAsnIleAspLeuGluGlyAsnValCysLeuAsnIleLeuArgGluAspTrpLys | 120 |
| | Qy | 361 | CCAGTCCTTACGATAAACTCCATAATTTATGGCCTGCAGTATCTCTTCTTGGAGCCCAAC | 420 |
| , | Db | 121 | ProValLeuThrIleAsnSerIleIleTyrGlyLeuGlnTyrLeuPheLeuGluProAsn | 140 |
| | Qy | 421 | CCCGAGGACCCACTGAACAAGGAGGCCGCAGAGGTCCTGCAGAACAACCGGCGGCTGTTT | 480 |
| | Db | 141 | ProGluAspProLeuAsnLysGluAlaAlaGluValLeuGlnAsnAsnArgArgLeuPhe | 160 |
| | Qy | 481 | GAGCAGAACGTGCAGCGCTCCATGCGGGGTGGCTACATCGGCTCCACCTACTTTGAGCGC | 540 |
| • | Db | 161 | GluGlnAsnValGlnArgSerMetArgGlyGlyTyrIleGlySerThrTyrPheGluArg | 180 |
| | Qy _. | 541 | TGCCTGAAA 549 | |
| | Db | 181 | CysLeuLys 183 | |
| | | | • | |
| | | | | |
| | • | | | |
| | | | | |